# AUTHOR INDEX

## to Volume 118, January–April 1988


Akam, M., 665
Albertson, M. C., 519
Alton, A. K., 235
Amato, G. D., 671
Ashley, T., 307

Baillie, D. L., 49
Barsel, S.-E., 637
Beaton, A. H., 247
Beckwith, J., 571
Benson, N., 21
Bentzen, P., 509
Benz, W. K., 461
Bethards, L. A., 149
Birchman, R., 425
Bode, V. C. J., 299
Bonhomme, F., 131
Braedt, G., 561
Brewer, K. L., 581
Britton-Davidian, J., 131
Brody, T., 329
Bronson, R., 693
Brown, G. G., 509
Burr, B., 519
Burr, F. A., 519
Byrne, B. J., 619

Caccone, A., 671
Campos-Ortega, J. A., 499
Chakraborty, R., 527
Chang, D.-Y., 593
Chovnick, A., 261
Ciampi, M. S., 193
Clark, A. G., 471
Clark, S. H., 261
Clarke, M., 425
Crow, J. F., 1, 389
Culbertson, M. R., 609

Dalton, D. K., 319
De Boer, J. G., 181
de la Concha, A., 499
Derman, A. I., 571
Devlin, R. H., 87
Diehl, W. J., 121
Dietrich, U., 499
Dietz, P. M., 619
Dove, W. F., 169, 389

Eberl, D. F., 109
Egorov, I. K., 287
Egorov, O. S., 287
Elliott, T., 581
Engels, W. R., 461

Fassler, J. S., 203
Fechtel, K., 235
Fink, G. R., 549
Fox, M. S., 5, 13
Friedman, D. B., 75
Fristrom, D., 247
Fristrom, J. W., 247
Fujimoto, R., 41
Futcher, B., 411

Garesse, R., 649
Gelman, R., 693
Gillespie, J. H., 385
Green, M. M., 221
Grigliatti, T. A., 87
Guenet, J.-L., 299

Hall, J. C., 267
Hamilton, E. P., 627
Hanson, M. R., 155
Hart, C. P., 319
Hartl, D. L., 537
Hastings, A., 543
Helentjaris, T., 353
Heschl, M. F. P., 49
Hickey, D. A., 411
Higgins, N. P., 581
Hilliker, A. J., 109, 261
Hilu, K. W., 155
Hoelzer, M. A., 31
Holm, D. G., 87
Hoogwerf, A. M., 665
Hunihan, L., 319
Hutchinson, F., 551

Iizuka, M., 365
Ishino-Arao, Y.41

James, S. W., 141
Jayaram, M., 393
Johnson, T. E., 75
Johnson-Schlitz, D., 461
Jorissen, L., 173
Judd, S. R., 401

Kayman, S. C., 425
Kiss, I., 247
Klittich, C. J. R., 417
Koehn, R. K., 121
Kuhn, D. T., 103
Kulkarni, S. J., 267

Langley, S. H., 319
Lebreton, B., 393
Lefebvre, P. A., 141, 637
Leggett, W. C., 509
Leslie, J. F., 417
Lu, A.-L., 593
Lyckegaard, E. M. S., 471

Maeda, N., 41
May, G., 213
McDonald, J. D., 299
McKim, K. S., 49
Meagher, T. R., 527
Meikle, S. B., 235
Michod, R. E., 31
Mills, D., 483
Mount, S. M., 221
Muskavitch, M. A. T., 235

Nadeau, J. H., 131
Nichols, L., 319

Ohno, Y., 41
Olson, M. V., 601
Ono, B.-I., 41
Orias, E., 627

Packert, G., 103
Palmer, J. D., 341
Pearson, R. K., 5, 13
Petes, T. D., 401
Phillis, R. W., 461
Pollak, E., 713
Powell, J. R., 671
Prasad, P. V., 393
Preston, C. R., 461

Ranum, L. P. W., 141
Reid, E., 411
Riddle, D. L., 61
Riggs, P. D., 571
Riles, L., 601
Ripley, L. S., 181
Roberts, D., 665
Robertson, A., 437, 445
Robertson, H. M., 461
Roderick, T. H., 319
Rogalski, T. M., 61
Rosenbluth, R. E., 49
Roth, J. R., 193
Rothenberg, M., 155
Rubin, G. M., 221
Ruddle, F. H., 319

# AUTHOR INDEX

## to Volume 118, January–April 1988


Akam, M., 665
Albertson, M. C., 519
Alton, A. K., 235
Amato, G. D., 671
Ashley, T., 307

Baillie, D. L., 49
Barsel, S.-E., 637
Beaton, A. H., 247
Beckwith, J., 571
Benson, N., 21
Bentzen, P., 509
Benz, W. K., 461
Bethards, L. A., 149
Birchman, R., 425
Bode, V. C. J., 299
Bonhomme, F., 131
Braedt, G., 561
Brewer, K. L., 581
Britton-Davidian, J., 131
Brody, T., 329
Bronson, R., 693
Brown, G. G., 509
Burr, B., 519
Burr, F. A., 519
Byrne, B. J., 619

Caccone, A., 671
Campos-Ortega, J. A., 499
Chakraborty, R., 527
Chang, D.-Y., 593
Chovnick, A., 261
Ciampi, M. S., 193
Clark, A. G., 471
Clark, S. H., 261
Clarke, M., 425
Crow, J. F., 1, 389
Culbertson, M. R., 609

Dalton, D. K., 319
De Boer, J. G., 181
de la Concha, A., 499
Derman, A. I., 571
Devlin, R. H., 87
Diehl, W. J., 121
Dietrich, U., 499
Dietz, P. M., 619
Dove, W. F., 169, 389

Eberl, D. F., 109
Egorov, I. K., 287
Egorov, O. S., 287
Elliott, T., 581
Engels, W. R., 461

Fassler, J. S., 203
Fechtel, K., 235
Fink, G. R., 549
Fox, M. S., 5, 13
Friedman, D. B., 75
Fristrom, D., 247
Fristrom, J. W., 247
Fujimoto, R., 41
Futcher, B., 411

Garesse, R., 649
Gelman, R., 693
Gillespie, J. H., 385
Green, M. M., 221
Grigliatti, T. A., 87
Guenet, J.-L., 299

Hall, J. C., 267
Hamilton, E. P., 627
Hanson, M. R., 155
Hart, C. P., 319
Hartl, D. L., 537
Hastings, A., 543
Helentjaris, T., 353
Heschl, M. F. P., 49
Hickey, D. A., 411
Higgins, N. P., 581
Hilliker, A. J., 109, 261
Hilu, K. W., 155
Hoelzer, M. A., 31
Holm, D. G., 87
Hoogwerf, A. M., 665
Hunihan, L., 319
Hutchinson, F., 551

Iizuka, M., 365
Ishino-Arao, Y.41

James, S. W., 141
Jayaram, M., 393
Johnson, T. E., 75
Johnson-Schlitz, D., 461
Jorissen, L., 173
Judd, S. R., 401

Kayman, S. C., 425
Kiss, I., 247
Klittich, C. J. R., 417
Koehn, R. K., 121
Kuhn, D. T., 103
Kulkarni, S. J., 267

Langley, S. H., 319
Lebreton, B., 393
Lefebvre, P. A., 141, 637
Leggett, W. C., 509
Leslie, J. F., 417
Lu, A.-L., 593
Lyckegaard, E. M. S., 471

Maeda, N., 41
May, G., 213
McDonald, J. D., 299
McKim, K. S., 49
Meagher, T. R., 527
Meikle, S. B., 235
Michod, R. E., 31
Mills, D., 483
Mount, S. M., 221
Muskavitch, M. A. T., 235

Nadeau, J. H., 131
Nichols, L., 319

Ohno, Y., 41
Olson, M. V., 601
Ono, B.-I., 41
Orias, E., 627

Packert, G., 103
Palmer, J. D., 341
Pearson, R. K., 5, 13
Petes, T. D., 401
Phillis, R. W., 461
Pollak, E., 713
Powell, J. R., 671
Prasad, P. V., 393
Preston, C. R., 461

Ranum, L. P. W., 141
Reid, E., 411
Riddle, D. L., 61
Riggs, P. D., 571
Riles, L., 601
Ripley, L. S., 181
Roberts, D., 665
Robertson, A., 437, 445
Robertson, H. M., 461
Roderick, T. H., 319
Rogalski, T. M., 61
Rosenbluth, R. E., 49
Roth, J. R., 193
Rothenberg, M., 155
Rubin, G. M., 221
Ruddle, F. H., 319

Samson, M.-L., 685
Sawyer, S. A., 537
Scandalios, J. G., 149
Scott, D. M., 713
Scott, M. E., 713
Scott, T. M., 121
Shrimpton, A. E., 437, 445
Silfow, C. D., 141
Simon, D., 299
Smoller, D., 483
Smouse, P. E., 527
Snyder, L., 173
Soller, M., 329
Stein, J., 551
Steinlauf, A. F., 267
Stoddart, J. A., 705
Stuber, C. W., 519
Sugiono, P., 21, 581
Suhr-Jessen, P. B., 627

Takahata, N., 387
Tanner, A. P., 619
Tardiff, J., 247
Taylor, B. A., 319
Taylor, J. F., 705
Taylor, J. W., 213
Terry, A. L., 235
Thaler, L, 131
Thompson, K. H., 519
Tindall, K. R., 551
Tsuchiya, Y., 41

Usui, T., 41

Waples, R. S., 371
Watson, A., 693
Weber, D., 353
Wegnez, M., 685
Weigel, D., 499
Weller, J. I., 329
Wexler, D. E., 637
Winey, M., 609
Winston, F., 203
Wojciechowski, M. F., 31
Wright, S., 353

Yedvobnick, B., 483
Youderian, P., 21, 393, 581
Young, P., 483
Yunis, E., 693

# SUBJECT INDEX

## to Volume 118, January–April 1988


Aging
  chromosomal regions, correlation with longevity, mouse, 693
  mutation in *age-1* gene, life span and fertility, *Caenorhabditis elegans*, 75
*Agrobacterium tumefaciens*, organism choices, 549
Allele
  electrophoretically cryptic, model, increase in genetic variability, 365
  estimation of frequencies, isoloci, 371
  neurogenic locus *mastermind*, molecular analysis, *Drosophila melanogaster*, 483
  neutral, overdispersed molecular clock, 385, 387
  *white-apricot*, copia, *Drosophila melanogaster*, 221
Allozymes, H-2 polymorphisms and, natural populations, house mouse, 131
Amanitin-binding subunit, RNA polymerase II gene, *Caenorhabditis elegans*, 61
Amiprophos-methyl, *uni* linkage group, *Chlamydomonas reinhardtii*, 141
Aneuploides, whole-arm trisomy, gene expression, *Drosophila melanogaster*, 87
*Arabidopsis thaliana*, organism choices, 549
ATP synthase, mitochondrial gene in petunia, 155

*Bacillus subtilis*, DNA repair, evolution of transformation, 31
Bacteriophage *lambda*
  gamma-ray mutagenesis, 551
  packaging, DNA heterologies, 5, 13
  repressor binding, DNA sequence determinants, 21
Bacteriophage P22, *Salmonella* chromosome, locked-in Mu*d*-P22 prophages, packaging specific segments, 581
Bacteriophage T4
  replication frameshifts, 181
  *unf/alc* protein map, RNA polymerase gene, *Escherichia coli* mutations, 173
Behavior, reproductive, courtship song and *dissonance*, *Drosophila melanogaster*, 267
Bithorax-complex, paternal imprinting of inversion *Uab*$^1$, homeotic transformations, Drosophila, 103
*Brassica*, mitochondrial DNA, intraspecific variation, multicircularity, 341
Bristles, sternopleural bristle score, polygenic factors, *Drosophila melanogaster*, 437, 445

*Caenorhabditis elegans*, 49, 61, 75
Catalase, molecular basis for CAT-2 null phenotype, 149
Cauliflower, source of mitochondrial DNA, 341
*Chamaelirium luteum*, natural populations, parentage analysis, genetic markers, 527
*Chlamydomonas reinhardtii*, 141, 637
Chlorate, nitrate reduction mutants, *Fusarium moniliforme*, 417
Chloroplast, DNA, identification of "A" genome, finger millet, 163
Chromosome
  mapping: *see* Mapping
  rearrangements, RNA polymerase II gene, *Caenorhabditis elegans*, 61
  regions correlated with longevity, mouse, 693
  source of mitochondrial DNA, *Brassica*, 341
  third, sternopleural bristle effects, *Drosophila melanogaster*, 437, 445
  *X*-linked recessive lethal mutations, embryonic morphogenesis, *Drosophila melanogaster*, 109
Chromosome *11*, *Hox-2* homeo box gene complex, mouse, 319
Chromsome *II*, *rose-gespleten* region, *Drosophila melanogaster*, 665
Ciliary plaques, *Paramecium tetraurelia*, paranoiac and related mutants, phenotypic characterization, 619
Clock
  episodic, 387
  molecular, neutral allele theory, evolution, 385
Conjugation, pronuclear fusion failure, vinblastine, *Tetrahymena thermophila*, 627
Copia, *white-apricot* allele, transposeable element, *Drosophila melanogaster*, 221
*Coprinus cinereus*, mating patterns, mitochondrial DNA inheritance, 213
Cytogenetics, *Delta* gene and neurogenesis, *Drosophila melanogaster*, 235
Cytosine, T4 *unf/alc* protein map, RNA polymerase gene, *Escherichia coli* mutations, 173

*Dictyostelium discoideum*, pleiotropic effects of motility, discoidin I regulation, 425
Disequilibrium, two-locus mutation-selection balance models, 543
DNA
  chloroplast, identification of "A" genome, finger millet, 163
  heterologies, bacteriophage λ packaging, 5, 13
  mismatch repair, *Escherichia coli*, 593
  mitochondrial
    gene organization, *Drosophila melanogaster*, 649
    length and restriction site heteroplasmy, American shad, 509
    mating patterns, *Coprinus cinereus*, 213
    segregation, *Drosophila melanogaster*, 471
    source of, *Brassica*, 341

IS*1*-dependent deletions, recombination, *Escherichia coli*, 561
unrelated, togetherness in genome, *Escherichia coli*, 537
Isoloci, estimation of allele frequencies, 371
Isozymes
molecular basis for CAT-2 null phenotype, maize, 149
quantitative trait loci, tomato, 329

Lifespan, chromosomal regions, correlation with longevity, mouse, 693
Locus
*Broad-Complex*, developmental effects, *Drosophila melanogaster*, 247
disequilibrium, two-locus mutation-selection balance models, 543
isoloci, estimation, allele frequencies, 371
*mastermind*, molecular analysis, *Drosophila melanogaster*, 483
quantitative trait loci, tomato, 329
*rosy*, recombination, *Drosophila melanogaster*, 261
Longevity
chromosomal regions, mouse, 693
mutation in *age-1* gene, *Caenorhabditis elegans*, 75

Maize
molecular basis for CAT-2 null phenotype, 149
recombinant inbreds, gene mapping, 519
Major histocompatibility complex, new mutations, mouse, 287
Mapping
first chromosome map, diamond anniversay, *Drosophila melanogaster*, 1
*Hox-2*, chromosome 11, mouse, 319
recombinant inbreds in maize, 519
*Salmonella* chromosome, locked-in Mud-P22 prophages, packaging specific segments, 581
third chromosome bristle effects, *Drosophila melanogaster*, 445
T4 *unf/alc* protein in RNA polymerase gene, *Escherichia coli*, 173
*unc-60* region, *Caenorhabditis elegans*, 49
Mating, patterns of, mitochondrial DNA inheritance, *Coprinus cinereus*, 213
Meiosis, synapsis and crossing over, G-band position effects, mouse, 307
Meiotic drive, evolution, segregation distortion, 389
Metamorphosis, *Broad-Complex* developmental effects, mutations, *Drosophila melanogaster*, 247
Methylation, DNA mismatch repair, *Escherichia coli*, 593
Microtubules
herbicides, *uni* linkage group, *Chlamydomonas reinhardtii*, 141
pronuclear fusion failure, vinblastine, *Tetrahymena thermophila*, 627
Millet, "A" genome, chloroplast DNA, 163
Mitochondria
ATP synthase proteolipid gene, petunia somatic hybrid, 155
DNA
scnDNA and, *Drosophila melanogaster*, 671
source of, *Brassica*, 341
DNA and gene organization, evolution, *Drosophila melanogaster*, 649
DNA inheritance, mating patterns, *Coprinus cinereus*, 213
Mobile element, maintenance of 2μm circle plasmid, sexual transmission, yeast, 411
Molecular clock: *see* Clock
Monoclonal antibodies, new MHC mutations, mouse, 287
Morphogenetics, *Delta* gene and neurogenesis, *Drosophila melanogaster*, 235
Motility, pleiotropic effects, discoidin I regulation, *Dictyostelium discoideum*, 425
Mouse
chromosomal regions, correlation, longevity, 693
*Drosophila* genetics, 169
G-band position effects, meiotic synapsis and crossing over, 307
H-2 and allozyme polymorphisms, natural populations, 131
hereditary hyperphenylalaninemia, *hph-1*, ethylnitrosourea mutagenesis, 299
*Hox-2* genetic mapping, 319
new MHC mutations, 287
*Mulinia lateralis*, heterozygosity and growth rate, glycolysis and protein catabolism, 121
Mutagenesis
ethylnitrosourea, hereditary hyperphenylalaninemia, mouse, 299
gamma-ray, *lambda* phage and prophage, 551
Mutants
*age-1* gene, life span and fertility, *Caenorhabditis elegans*, 75
*Drosophila melanogaster*
*dissonance*, courtship ship, 267
recombination, *rosy* locus, 261
long-flagella, genetic analysis, *Chlamydomonas reinhardtii*, 637
paternal imprinting of inversion *Uab*$^1$, homeotic transformations, Drosphila, 103
*X*-linked recessive lethal mutations, embryonic morphogenesis, *Drosophila melanogaster*, 109
Mutations
*Broad-Complex*, developmental effects, *Drosophila melanogaster*, 247
DNA sequence determinants, λ repressor binding, 21
episodic clock, 387
*Escherichia coli*, T4 *unf/alc* protein, RNA polymerase gene, 173
frameshift, assay, bacteriophage T4, 181
nonsense, essential genes, yeast, 601

repair, evolution of transformation, *Bacillus subtilis*, 31
*Salmonella* chromosome, locked-in Mud-P22 prophages, packaging specific segments, 581
sequence determinants, λ repressor binding, 21
single-copy nuclear and mitochondrial, rates and patterns, *Drosophila melanogaster* subgroup, 671
DNA polymerase, assay for frameshift mutations, bacteriophage T4, 181
Dosage compensation, whole-arm trisomies, gene expression, *Drosophila melanogaster*, 87
*Drosophila melanogaster*, 1, 87, 109, 221, 235, 247, 261, 267, 389, 437, 445, 461, 471, 483, 499, 549, 649, 665, 671, 685
*Drosophila pseudoobscura*, 389

Ecdysone, *Broad-Complex* developmental effects, mutations, *Drosophila melanogaster*, 247
Embryogenesis
*Delta* gene and neurogenesis, *Drosophila melanogaster*, 235
*X*-linked recessive lethal mutations, *Drosophila melanogaster*, 109
Equilibrium, mean fertility maximum, 713
*Escherichia coli*, 173, 537, 549, 551, 561, 571, 593
Estimation, prediction in samples, genotypic diversity, 705
*N*-Ethyl-*N*-nitrosourea, hereditary hyperphenylalaninemia, *hph-1*, mouse, 299
Evolution
bipartite structure, 5S ribosomal gene family, *Drosophila melanogaster*, 685
duplicate nucleotide sequences, restriction fragment length polymorphisms, maize, 353
identification of "A" genome, chloroplast DNA, finger millet, 163
meiotic drive, segregation distortion, 389
mitochondrial DNA, gene organization, *Drosophila melanogaster*, 649
overdispersed molecular clock, 385, 387
source of mitochondrial DNA, *Brassica*, 341
transformation, DNA repair, *Bacillus subtilis*, 31

Fertility
life span and, *age-1* gene, *Caenorhabditis elegans*, 75
pronuclear fusion failure, vinblastine, *Tetrahymena thermophila*, 627
stable equilibrium maximum points, 713
Flagella, long, genetic analysis of mutants, *Chlamydomonas reinhardtii*, 637
FLP recombinase, yeast, substrate binding, mutations, 393
*Fusarium moniliforme*, nitrate reduction mutants, 417

Gamma rays, mutagenesis, *lambda* phage and prophage, 551
G-bands, position effects on meiotic synapsis, crossing over, mouse, 307
Gene
*age-1*, life span and fertility, *Caenorhabditis elegans*, 75
CAT-2 null phenotype, molecular basis, maize, 149
conversion, lengths of tracts, yeast, 401
*Delta*, neurogenesis, *Drosophila melanogaster*, 235
essential
lethal mutations, *Caenorhabditis elegans*, 61
nonsense mutations, yeast, 601
*hisG*, polarity effects, *Salmonella typhimurium*, 193
*Lsp-2*, *rose-gespleten* region, *Drosophila melanogaster*, 665
neurogenic, functional interactions, *Drosophila melanogaster*, 499
regulatory, whole-arm trisomy, *Drosophila melanogaster*, 87
*sec*, regulation of *secA-lacZ* fusion, *Escherichia coli*, 571
5S ribosomal family, bipartite structure, *Drosophila melanogaster*, 685
transversion mismatch repair, *Escherichia coli*, 593
*unc-60* region, *Caenorhabditis elegans*, 49
Genome
"A", chloroplast DNA, finger millet, 163
*Arabidopsis thaliana*, organism choices, 549
restriction fragment length polymorphisms, duplicate nucleotide sequences, maize, 353
stable source of *P* element transposase, *Drosophila melanogaster*, 461
unrelated insertion sequences, *Escherichia coli*, 537
Genotypic diversity, estimation and prediction in samples, 705
Glycolysis, protein catabolism and, heterozygosity and growth, *Mulinia lateralis*, 121

H-2 complex
allozyme polymorphisms and, natural populations, house mouse, 131
new MHC mutations, mouse, 287
Herbicides, anti-microtubule, resistant mutants, *Chlamydomonas reinhardtii*, 141
Heterology, DNA, bacteriophage λ packaging, 5, 13
Heteroplasmy, length and restriction site, mitochondrial DNA, American shad, 509
Heterozygosity, glycolysis and protein catabolism, *Mulinia lateralis*, 121
Homeo box, *Hox-2* genetic mapping, mouse, 319
Hybridization, scnDNA and mtDNA, rates and patterns, *Drosophila melanogaster*, 671
Hyperphenylalaninemia, hereditary, ethylnitrosourea mutagenesis, mouse, 299

Imaginal discs, *Broad-Complex* developmental effects, mutations, *Drosophila melanogaster*, 247
Imprinting, paternal, inversion *Uab*$^{1}$, Drosophila transformations, 103
Insertion sequences

regulation of *secA-lacZ* fusion, new *sec* gene, *Escherichia coli*, 571
tRNA-splicing endonuclease activity, yeast, 609
Ty insertion elements, yeast, 203

*Nasonia vitripennis*, 389
Neoplasia, *Drosophila* genetics, 169
Neurogenesis
*Delta* gene, *Drosophila melanogaster*, 235
functional interactions of neurogenic genes, *Drosophila melanogaster*, 499
locus *mastermind*, molecular analysis, *Drosophila melanogaster*, 483
Nitrate, reduction mutants, *Fusarium moniliforme*, 417
Nucleotides, duplicate sequences, restriction fragment length polymorphisms, maize, 353

Oryzalin, *uni* linkage group, *Chlamydomonas reinhardtii*, 141

*Paramecium tetraurelia*, paranoiac and related mutants, phenotypic characterization, 619
Paternity, parentage analysis with genetic markers, natural populations, *Chamaelirium luteum*, 527
*P* element transposase, stable genomic source, *Drosophila melanogaster*, 461
Petunia, mitochondrial gene, 155
Phenylketonuria, hereditary hyperphenylalanine, ethylnitrosourea mutagenesis, mouse, 299
Phylogeny, H-2 and allozyme polymorphisms, natural populations, house mouse, 131
Polarity, *hisG* gene, *Salmonella typhimurium*, 193
Polymorphism
electrophoretically cryptic allele, model, increase in genetic variability, 365
glycolysis and protein catabolism, heterozygosity and growth, *Mulinia laterali*, 121
length and restriction site, mitochondrial DNA, American shad, 509
restriction fragment length, duplicated loci, maize, 353
Population
mean fertility maximum, stable equilibrium, 713
natural
H-2 and allozyme polymorphisms, house mouse, 131
parentage analysis and genetic markers, *Chamaelirium luteum*, 527
Prediction, estimation, samples, genotypic diversity, 705
Protein
catabolism, locus-specific growth effects, *Mulinia lateralis*, 121
export, *secA-lacZ* fusion, *Escherichia coli*, 571
yeast FLP recombinase, substrate binding, mutations, 393

Quantitative traits, linkage analysis, tomato, 329

Radiation, gamma-ray mutagenesis, *lambda* phage and prophage, 551
Recombination
disequilibrium, two-locus mutation-selection balance models, 543
DNA heterologies, bacteriophage λ packaging, 13
initiation and termination, *rosy* locus, *Drosophila melanogaster*, 261
IS*1*-dependent deletions, *Escherichia coli*, 561
mitochondrial ATP synthase proteolipid gene, petunia somatic hybrid, 155
yeast FLP recombinase, substrate binding, mutations, 393
Repressor, λ, binding, DNA sequence determinants, 21
Reproduction
courtship song, *dissonance* mutant, *Drosophila melanogaster*, 267
life span and fertility, *age-1* gene, *Caenorhabditis elegans*, 75
*Rho* factor, polarity effects of *hisG* gene, *Salmonella typhimurium*, 193
tRNA, -splicing endonuclease activity, mutations, yeast, 609
RNA polymerase, T4 *unf/alc* protein, *Escherichia coli* mutations, 173
RNA polymerase II, *ama-1 IV*, *Caenorhabditis elegans*, 61

*Saccharomyces cerevisiae*, 41, 203, 393, 401, 411, 549, 601, 609
*Salmonella typhimurium*, 193, 581
Segregation, mtDNA and, natural selection, *Drosophila melanogaster*, 471
Segregation distortion, meiotic drive and evolution, 389
Sex
evolution of, *Bacillus subtilis*, 31
maintenance of 2μm circle plasmid, yeast, 411
pronuclear fusion failure, vinblastine, *Tetrahymena thermophila*, 627
Sexual cycle, organism choices, 549
Shad, length and restriction site heteroplasmy, mitochondrial DNA, 509
Skin grafts, new MHC mutations, mouse, 287
Song, *dissonance* mutant, courtship, *Drosophila melanogaster*, 267
Suppressors
ochre, nonsense mutations, yeast, 601
Ty insertion mutations, yeast, 203
UGA, yeast, 41
Synapsis, meiotic, G-band position effects, mouse, 307

*Tetrahymena thermophila*, pronuclear fusion failure, conjugational pathway, vinblastine, 627
Tomato, quantitative trait loci, 329
Transformation, evolution of, DNA repair, *Bacillus subtilis*, 31

Transposable element, *white-apricot* allele, partial revertants, *Drosophila melanogaster*, 221
Transposition, *Salmonella* chromosome, locked-in Mu*d*-P22 prophages, packaging specific segments, 581
Trisomy, whole-arm, gene expression, *Drosophila melanogaster*, 87
Tubulin, anti-microtubule herbicides, *uni* linkage group, *Chlamydomonas reinhardtii*, 141
Tumor, transplantation, new MHC mutations, mouse, 287
Ty elements, novel class of suppressor, insertion mutations, yeast, 203

Vinblastine, pronuclear fusion failure, conjugational pathway, *Tetrahymena thermophila*, 627

*Xanthine dehydrogenase*, electrophoretically cryptic allele, model, increase in genetic variability, 365

Yeast
binding of FLP recombinase to its substrate, mutations, 393
maintenance of 2μm circle plasmid, sexual transmission, 411
nonsense mutations in essential genes, 601
organism choices, 549
physical lengths, meiotic and mitotic gene conversion, 401
tRNA-splicing endonuclease activity, mutations, 609
Ty insertion mutations, suppressor class, 203
UGA suppressors, 41